Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

We claim:

Claims 1-18 (Cancelled)

Claim 19. (New) A gene signature predictive of patient response or outcome to anti-estrogen therapy for recurring breast cancer, comprising two or more marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$.

Claim 20. (New) The gene signature of claim 19, wherein said marker genes are selected from the 81-gene signature listed in Table 1.

Claim 21. (New) The gene signature of claim 19, wherein said marker genes are selected from the 44-gene signature listed in Table 1.

Claim 22. (New) The gene signature of claim 19, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, DEME-6, TNC, and COX-6C.

Claim 23. (New) The gene signature of claim 19, wherein said marker genes comprise at least one of TNC, SIAH-2, DEME-6, and COX-6C.

Claim 24. (New) The gene signature of claim 19, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, and DEME-6.

Claim 25. (New) The gene signature of claim 19, wherein said marker genes comprise at least one of CASP-2 and DEME-6, and at least one of SIAH-2 and TNC.

Claim 26. (New) An assay system for predicting patient response or outcome to anti-estrogen therapy for recurring breast cancer configured and adapted to detect the gene signature of claim 19, comprising:

a) two or more marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$;

b) two or more nucleic acid probes, comprising at least 10 to 50 contiguous nucleic acids of marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$, or complementary nucleic acid sequences thereof; or

c) two or more binding ligands that specifically detect polypeptides encoded by marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$.

Claim 27. (New) The assay system of claim 26, wherein said marker genes are selected from the 81-gene signature listed in Table 1.

Claim 28. (New) The assay system of claim 26, wherein said marker genes are selected from the 44-gene signature listed in Table 1.

Claim 29. (New) The assay system of claim 26, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, DEME-6, TNC, and COX-6C.

Claim 30. (New) The assay system of claim 26, wherein said marker genes comprise at least one of TNC, SIAH-2, DEME-6, and COX-6C.

Claim 31. (New) The assay system of claim 26, wherein said marker genes comprise at least one of FN-1, CASP-2, THRAP-2, SIAH-2, and DEME-6.

Claim 32. (New) The assay system of claim 26, wherein said marker genes comprise at least one of CASP-2 and DEME-6, and at least one of SIAH-2 and TNC.

Claim 33. (New) The assay system of claim 26, wherein said marker genes, nucleic acid probes, or binding ligands are disposed on an assay surface.

Claim 34. (New) The assay system of claim 26, wherein said assay surface comprises a chip, array, or fluidity card.

Claim 35. (New) The assay system of claim 26, wherein said probes comprise complementary nucleic acid sequences to at least 10 to 50 nucleic acid sequences of said marker genes.

Claim 36. (New) The assay system of claim 26, wherein said binding ligands comprise antibodies or binding fragments thereof.

Claim 37. (New) A method for predicting outcome of anti-estrogen therapy for recurrent breast cancer, the method comprising:

a) analyzing a patient's primary tumor for expression of two or more marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$;

b) determining if the expression pattern of said tumor's marker genes correlates with a Cluster 1 or Cluster 2 expression pattern; and

c) correlating a Cluster 1 expression pattern with prediction of Progressive Disease and a Cluster 2 expression pattern with Objective Response to anti-estrogen therapy for recurrent breast cancer.

Claim 38. (New) The method of claim 37, wherein said primary tumor is analyzed for expression of the 81-gene signature or the 44-gene signaure listed in Table 1.

Claim 39. (New) A method for predicting Progression Free Survival of anti-estrogen therapy for recurrent breast cancer, the method comprising:

a) analyzing a patient's primary tumor for expression of two or more marker genes identified in Table 1 as differentially expressed in primary tumors of recurring breast cancer patients exhibiting an outcome to anti-estrogen therapy with a significance of $p \leq 0.05$;

b) determining if the expression pattern of said tumor's marker genes correlates with a Cluster 1 or Cluster 2 expression pattern; and

c) correlating a Cluster 1 expression pattern with a negative prediction of Progression Free Survival for recurrent breast cancer and a Cluster 2 expression pattern with a positive Progression Free Survival for recurrent breast cancer.

Claim 40. (New) The method of claim 39, wherein said primary tumor is analyzed for expression of the the 81-gene signature or the 44-gene signaure listed in Table 1.

Abstract:

Please insert the following abstract into the application as the last page thereof.

Gene signatures, specific marker genes, and diagnostic assays for predicting progression free survival and objective response to anti-estrogen, e. g., tamoxifen therapy for recurring breast cancer patients are described.